

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/502,498A

CRF Processing Date: 1/30/2003

Edited by: AL

Verified by: AL (STIC staff)

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

## RAW SEQUENCE LISTING

DATE: 01/30/2003

PATENT APPLICATION: US/09/502,498A

TIME: 12:42:55

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\01292003\I502498A.raw

3 <110> APPLICANT: Kilian, Andrzej  
 4 Bowtell, David  
 6 <120> TITLE OF INVENTION: VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES  
 7 THEREOF  
 9 <130> FILE REFERENCE: 082447-0102  
 11 <140> CURRENT APPLICATION NUMBER: 09/502,498A  
 12 <141> CURRENT FILING DATE: 2000-02-11  
 14 <160> NUMBER OF SEQ ID NOS: 155  
 16 <170> SOFTWARE: PatentIn Ver. 2.0  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 3964  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Homo sapiens  
 23 <400> SEQUENCE: 1  
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 26 cgcggggacc cggcggcttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180  
 27 gacgcacggc cccccccgc cccccctcc ttccgccagg tgctctgcct gaaggagctg 240  
 28 gtggcccagag tgctgcagag gctgtgcgag cgcggcgcca agaactgctt ggcttccggc 300  
 29 ttgcgcgctg tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
 30 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgct ggggctgctg 420  
 31 ttgcgcgctg tggcgacgca cgtgctggtt cactctgctg cagcgtgcgc gctctttgtg 480  
 32 ctggtggctc ccagctgcgc ctaccagggt tgcgggccgc cgctgtacca gctcggcgct 540  
 33 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgctt gggatgcgaa 600  
 34 cgggcctgga accatagcgt cagggaggcc ggggtcccc tgggcctgcc agccccgggt 660  
 35 gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gccaggcgct 720  
 36 ggcgctgcc ctgagccgga gcggacgcc gttgggcagg ggtcctgggc ccaccggggc 780  
 37 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cactgccag acccgccgaa 840  
 38 gaagccacct ctttgagggt tgcgctctct ggcacgcgcc actcccaccc atccgtgggc 900  
 39 cgccagcacc acgcggggcc cccatccaca tcgcggccac cagctccctg ggacacgcct 960  
 40 tgtcccccg tgtaacccga gaccaagcac ttctctact cctcaggcga caaggagcag 1020  
 41 ctgcggccct ccttctact cagctctctg aggccagcc tgactggcg tcggaggctc 1080  
 42 gtggagacca tctttctggg ttccaggccc tggatgccag ggactcccc caggttgccc 1140  
 43 cgctgcccc agcgtactg gcaaatgcgg cccctgtttc tggagctgct tgggaaccac 1200  
 44 gcgcagtgcc cctacggggt gtcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260  
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 49 gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcggggctg cgcttggtg 1560  
 50 gcgaggagcc caggggttg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620  
 51 ctggccaagt tcctgcactg gctgatgagt gtgtacgtcg tcgagctgct cagggtctttc 1680  
 52 ttttatgtca cggagaccac gtttcaaaa aacaggctct ttttctaccg gaagagtgtc 1740

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Output Set: N:\CRF4\01292003\I502498A.raw

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55 ctccgcttca tccccaaagg tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920
56 ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980
57 ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgcctctgtg 2040
58 ctgggcctgg acgatatcca cagggcctgg cgcaccttgc tgctgcgtgt gcgggcccag 2100
59 gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160
60 cccaggaca ggctcacgga ggtcatcgcc agcatcatca aaccccagaa caggtactgc 2220
61 gtgcgtcggg atgccgtggg ccagaaggcc gcccatgggc acgtccgcaa ggctttcaag 2280
62 agccacgtct ctacctgac agacctccag ccgtacatgc gacagttcgt ggctcacctg 2340
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67 gggctgctcc tgcgtttggg ggtatgattt ttgttggtga cacctcacct caccacgcg 2640
68 aaaaccttcc tcaggacctt ggtccgaggt gtccctgagt atggctgcgt ggtgaacttg 2700
69 cggaagacag tgggtgaact ccctgtagaa gacgaggccc tgggtggcac ggcttttgtt 2760
70 cagatgccgg cccacggcct attcccctgg tgcggcctgc tgctggatac ccggaccctg 2820
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77 gccgcccggc ctctgccctc cgaggccgtg cagtggctgt gccaccaagc attcctgctc 3240
78 aagctgactc gacaccgtgt cacctacgtg ccactcctgg ggtcactcag gacagcccag 3300
79 acgcagctga gtcggaagct cccggggacg acgtgactg ccctggaggc cgcagccaac 3360
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84 gggctgagtg tccagcacac ctgccgtctt cacttcccca caggctggcg ctgggtcca 3660
85 cccaggggcc agcttttctt caccaggagc ccggcttcca ctcccacat aggaatagtc 3720
86 catccccaga ttcgccattg ttacccctc gccctgccct cctttgcctt ccacccccac 3780
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88 gtgtgccctg tacacaggcg aggaccctgc acctggatgg gggccctgt gggtcaaatt 3900
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90 aaaa 3964

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92 &lt;210&gt; SEQ ID NO: 2

93 &lt;211&gt; LENGTH: 1132

94 &lt;212&gt; TYPE: PRT

95 &lt;213&gt; ORGANISM: Homo sapiens

97 &lt;400&gt; SEQUENCE: 2

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98 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
99 1 5 10 15
101 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
102 20 25 30
104 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
105 35 40 45

```

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Input Set : A:\PTO.AMC.txt

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107 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
108      50      55      60
110 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
111 65      70      75      80
113 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
114      85      90      95
116 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
117      100      105      110
119 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
120      115      120      125
122 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Arg Arg Val
123      130      135      140
125 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
126 145      150      155      160
128 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
129      165      170      175
131 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
132      180      185      190
134 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
135      195      200      205
137 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
138      210      215      220
140 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
141 225      230      235      240
143 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
144      245      250      255
146 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
147      260      265      270
149 Val Ser Pro Ala Arg Pro Ala Glu Ala Thr Ser Leu Glu Gly Ala
150      275      280      285
152 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
153      290      295      300
155 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
156 305      310      315      320
158 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
159      325      330      335
161 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
162      340      345      350
164 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
165      355      360      365
167 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
168      370      375      380
170 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
171 385      390      395      400
173 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
174      405      410      415
176 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
177      420      425      430
179 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu

```

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```

180          435          440          445
182 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
183          450          455          460
185 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
186 465          470          475          480
188 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
189          485          490          495
191 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
192          500          505          510
194 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
195          515          520          525
197 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
198          530          535          540
200 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
201 545          550          555          560
203 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
204          565          570          575
206 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
207          580          585          590
209 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
210          595          600          605
212 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
213          610          615          620
215 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
216 625          630          635          640
218 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
219          645          650          655
221 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
222          660          665          670
224 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
225          675          680          685
227 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
228          690          695          700
230 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
231 705          710          715          720
233 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
234          725          730          735
236 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
237          740          745          750
239 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
240          755          760          765
242 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
243          770          775          780
245 Pro Leu Arg Asp Ala Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
246 785          790          795          800
248 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
249          805          810          815
251 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
252          820          825          830

```

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Output Set: N:\CRF4\01292003\I502498A.raw

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254 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
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257 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
258      850      855      860
260 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
261 865      870      875      880
263 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
264      885      890      895
266 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
267      900      905      910
269 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
270      915      920      925
272 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
273      930      935      940
275 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
276 945      950      955      960
278 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
279      965      970      975
281 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
282      980      985      990
284 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
285      995      1000      1005
287 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
288      1010      1015      1020
290 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
291 1025      1030      1035      1040
293 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
294      1045      1050      1055
296 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
297      1060      1065      1070
299 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
300      1075      1080      1085
302 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
303      1090      1095      1100
305 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
306 1105      1110      1115      1120
308 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
309      1125      1130
312 <210> SEQ ID NO: 3
313 <211> LENGTH: 1031
314 <212> TYPE: PRT
315 <213> ORGANISM: Euplotes aediculatus
317 <400> SEQUENCE: 3
318 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
319 1 5 10 15
321 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
322 20 25 30
324 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
325 35 40 45

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/502,498A

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Input Set : A:\PTO.AMC.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 1,2,3,4,5,6,7  
Seq#:34; N Pos. 1767,1768,1769  
Seq#:51; N Pos. 1871,1872,1873  
Seq#:91; Xaa Pos. 2,3,4,5  
Seq#:93; Xaa Pos. 2,3,4,5,7,8  
Seq#:95; N Pos. 1,2,3,5,9,10,11,12,13,14